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AL169302 Tetraodon
AL213956 Tetraodon
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ALIGNMENTS

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	JOURNAL MEDLINE COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AW531158 LOCUS DEFINITION
University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Fal: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through	discovery Genome Res. 6 (9), 791-806 (1996) 97044477 Contact: Soares, MB	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 413) 1 (bases 1 to 413) 1 Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene	UI-R-BT1-akv-d-05-0-UI 3', mRNA sequence. AW531158 AW531158.1 GI:7173572 EST. ROTWAY rat. ROTWAY rat. Rattus norveoicus	AW531158 413 bp mRNA linear EST 06-MAR-2000 UI-R-BT1-akv-d-05-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone

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Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab
clones will be available through Research
                                                                                                    Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                       451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                    BF563910 437 bp mRNA UI-R-BT1-akv-d-05-0-UI.rl UI-R-BT1 Rattus UI-R-BT1-akv-d-05-0-UI 5', mRNA sequence.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library UI-R-BFI is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.liowa.edu. The subtraction has been previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=lung
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TAG_LIB=UI-R-BT1
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                                                                                                                                                                                                            136;
                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                          Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ311551 674 bp mRNA linear RC2-BN0332-200600-011-d12 BN0332 Homo sapiens cDNA,
Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLNL (info@image.llnl.gov). IMAGE ID- 1800144 The following repetitive elements were found in this cDNA sequence: 379-429, >GC_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is also available through the I.M.A.G.E. Consortium LLNL (info@image.llnl.gov). IMAGE ID= 1800144 The following
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/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a mixture of
/note="Vector: pt773D-Pac (Pharmacia) with a mixture of
/note="Vector: Site_1: Not I; Site_2: Eco RI; The library
/note="Vector: Site_1: Not I; Site_2: Eco RI; The library
/note from a mixture of
/note="Vector: Site_1: Not I; Site_2: Eco RI; The library
/note from a mixture of
/note="Vector: Site_1: Not I; Site_2: Eco RI; The library from which this
/note from was derived, please visit our web site at
/note from the subtraction has been previously
/note from the subtraction has been previously
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/db_xref="taxon:10116"
/clone="UI-R-BT1-aky-d-05-0-UI"
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                                                                                                                                                               Acad. Sci. U.S.A. 97
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Pred. No. 1.9e-25;
0; Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
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High quality sequence stop: 671.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-BN0332-200600-011-d12&t3=2000-06-20&t4=1)
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                                                                                                                                                                                                                                 Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                       2 (bases 1 to 1040)
Roest-Crollius, H., J
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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1 (bases 1 to 1040)
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                    Genoscope
                                                                                                          Charaterization and repeat analysis of the compact genome of the
                                                                                                                              Weissenbach,J
                                                                                                                                                Bouneau, L., Billault, A., Quetier, F.,
                                                                                                                                                                                                             Unpublished
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/db_xref="taxon:9606"
/clone_lib="BN0332"
/dev_stage="Adult"
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library G from Tetraodon nigroviridis, genomic survey
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73.0%;
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Pred. No. 2.
                                                                                 Tetraodon nigroviridis
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2.3e-17;
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                                                                                                                                                     Saurin, W.,
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Euteleostei; Neoteleostei;
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                                                                                                                                                                         Fisher, C.,
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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                                                                                 This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizam
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases cal
v0.980904 e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                       PCR PRimers
                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
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/clone="166022"
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a 219 c 221 g 216 t
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       /tissue_type="pooled"
/lab_host="PH10B"
/lab_host="PH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2:
Library made from pooled tissue from lymph node, c
fat, hypothalamus, and pituitary."
155 c 140 g 101 t 1 others
                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
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                  2 CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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CACCGAGACCTCAAGTCCAACAACATTCTGCTGCTGCAGCCCATTGAAGGTGACGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed
v0.980904.e. Vector identified by cross_match with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 76 row: M column: 8
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
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181081 MARC 4BOV Bos taurus cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 551)
                                                                                                                                                  106
                                                                                                                                                                                                                                                                                                                                                                                              PRimers
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                                                                  Conservative
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                                                                                                                                                embryos.
a 169
                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2 Library made from pooled tissue from day 20 and embryos."
                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                             /clone_lib="MARC 4BOV"
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                                                                              51.6%;
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No. 5
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5.5e-15;
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RESULT 8
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  62 TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                                         2 CACCGGGACATCAAGGCAGGAAATATTTTGCTTACTTGAGAAGATAGAACATGATGACATC 61
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                                                        CACCGAGACCTCAAGTCCAACAACATTCTGCTGCTGCAGCCCATTGAAGGTGACGACATG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Dr. Chris Tuggle, Iowa State University cDNA Library preparation: Dr. M. Bento Soares, University of cDNA Library Arrayed by: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Resea Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ604135 791 bp mRNA lir
MI-P-CP1-nzb-a-19-0-UI.sl MI-P-CP1 Sus scrofa
MI-P-CP1-nzb-a-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tuggle CK Molecular Genetics Laboratory, Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
/organism="Crossbreed"
/db_xref="taxon:8823"
/db_xref="Mi-P-CP1"
/clone_lib="Mi-P-CP1"
/clone_Mi-P-CP1"
/lab host="JH10B (Life Technologies)"
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                                                                                                                                                                                                Score 84.6; DB 14
Pred. No. 6.2e-15;
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                                                                                                              CAAATGAGTGCCGCGGGCACCTACGCCTGGATGGCTCCTGAGG
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                                                                                                                                                                                                                                                            CACCGTGATCTCAAGTCCAACAACATTTTGCTGCTGCAGCCCATTGAGAGTGACGACATG 137
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BQ719600 873 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8234446 Lupski_sympathetic_trunk Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito, K., Yamamoto, J., Nak
,Y., Sugano, S., Isogai, T.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   /uore="Vector: pME18SFL3; mRNA from uninduced precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4001663"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="teratocarcinoma"
/cell_line="NT2"
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Pred. No. 1.8e-14;
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Nakamura,Y., Nishikawa,T., Nagai,T.,
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TITLE
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                                                                                                                                                                                                                                                                                              62 TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                        CAAATGAGTGCCGCGGGCACCTACGCCTGGATGGCTCCTGAGG
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                                                                        5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Homo sapiens
                                                       BQ227232.1
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Plate: LLAM13584 row: l column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                     human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylc College of Medicine); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGGGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6188692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Lupski_sympathetic_trunk"
/sex="male"
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Pred. No. 1.9e-14;
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REFERENCE
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Matches 113; Conserv
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AGENCOURT 6554238 NIH_MGC_72
5', mRNA sequence.
BM5449522
                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1057)
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Plate: LLAM13328 row: n column: 09
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informat.
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through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo and Average insert size 1.8 kb. Library constructed by L Technologies."
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/clone_lib="NIH_MGC_68"
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Tissue Procurement: Dr. Mark Watson
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National Institutes of Health, /
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/clone="IMAGE:5548665"
/clone=lib="NIH_MGC_72"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the
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                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6215047"
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACCAAAATG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG751808
BG751808.1 GI:14062461
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLCM1753 row: j column: High quality sequence stop: 856.
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National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG751808
   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                            adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "

276 c 280 g 140 t
                                                                                                                                                                                                                                                                                                                        /Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4874218"
/clone=!b="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal"
/tis
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45.9%;
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Score
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Pred. No. 4.7e-13;
0; Mismatches 49;
75.2; DB 12;
No. 4.4e-12;
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                               Length 863;
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VERSION
KEYWORDS
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BQ266193
LOCUS
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Best Local Similarity
Matches 108; Conserv
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354 GAACACAAGACCCTAAAGATTACTGACTTCGGCCTCGCCCGAGAGTGGCACAAAACCACC
                                                                    294 CACCGAGACCTGAAGTCCAACAACATTCTGTTGCTGCAGCCCATCGAGGGTGACGACATG 353
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                             62 TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
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                                                                                           2 CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGATGACATC 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen/Robin Humphreys
CDNA Library Preparation: Life Technologies
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information car
info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATCTGCAATAAAACTTTTGAAGA
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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BQ266193.1 GI:20491258
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Location/Qualifiers
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NISC_fflle05.yl NCI_CGAP_Mam5
5', mRNA sequence.
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                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                               45.78;
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                                                                                                                                             Score 75; DB : Pred. No. 4.1e 0; Mismatches
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5 Mus musculus cDNA clone IMAGE:2865512
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tches 55;
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414 CAGATGAGTGCTGCGGGCACCTACGCTTGGATGGCTCCCGAGG
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 456
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Search completed: December 13, 2002, 23:27:10 Job time: 2181 secs